

## Original Research Article

# Exploring Genetic Distance and Diversity Analysis in Okra (*Abelmoschus esculentus* L. Moench): A Comprehensive Study on the Genetic Variation within Cultivars

### Abstract

Okra (*Abelmoschus esculentus* L.), an important vegetable crop, is recognized for its nutritional, medicinal, and economic significance. This study explores the genetic diversity among 28 okra genotypes, focusing on traits such as plant height, fruit yield, and seed weight, which are essential for crop improvement. Genetic variability, heritability, and principal component analysis (PCA) were employed to evaluate the genotypes. Results revealed significant variability, with high heritability estimates for traits like plant height and fruit yield, indicating the predominance of additive genetic effects. Genetic diversity ranged from 0.19 to 4.09, with the greatest distance observed between G1 and G28, suggesting their potential as parents for hybridization. PCA identified five principal components explaining 80.67% of the total variation, emphasizing the contribution of plant height, fruit weight, and seeds per pod to genetic divergence. Genotypes such as G1 and G18 were identified for early maturity and high yield, while G6 and G20 were selected for lower seed content, making them suitable for breeding programs. The findings underscore the importance of genetic diversity in developing high-yielding, resilient okra varieties and provide a framework for future breeding strategies.

**Keywords:** Euclidean distance, Diversity Analysis, Hybridization, Okra

### Introduction

Okra (*Abelmoschus esculentus* (L.) Moench) is known as lady's finger, Dherosh in Bangladesh, is a commercial vegetable crop and belongs to the family Malvaceae. Not only it has industrial value, but also it has both medicinal and nutritional values[1]. It has a vital role in human diet and is a good source of vitamin A, B, and C and also rich in protein, minerals and iodine [2]. The main origin of okra is Ethiopia and, then it is widely spreaded all over tropical, subtropical and warm temperate regions of the World[3]. Total area under okra cultivation in Bangladesh is estimated to be 30118.73 acres yielding about 70242.27 tons of green pods[4]. The average yield of okra in Bangladesh is 2332.28 Kg ac<sup>-1</sup> which is very low as compared to other okra growing countries. Improving okra productivity requires a comprehensive understanding of genetic diversity

within the crop's germplasm. Genetic diversity is crucial for breeding programs, as it enables the identification of genotypes with desirable traits such as high yield, early maturity, and pest resistance. Such diversity facilitates the selection of parents for hybridization and the development of transgressive segregants, ultimately enhancing crop improvement. Knowledge of inheritance patterns and variability in key traits provides the foundation for effective breeding strategies. This study aims to evaluate genetic variability, heritability, and genetic divergence among 28 okra genotypes collected from diverse sources. By identifying superior genotypes based on their agronomic traits and genetic parameters, this research contributes to the development of high-yielding, resilient okra varieties suitable for specific growing regions. The findings provide valuable insights into harnessing genetic diversity for sustainable okra production. At present time, enormous amount of commercial cultivars including F1 hybrids of okra is available in the market. But all these are not adapted and suited to all the regions of the country. Further, no specific recommendation about the suitability of genotypes for a particular area is available[5]. Genetic diversity knowledge within okra germplasms play significant role in breeding program. This helps to develop varieties with desired traits. Most importantly it is a prerequisite to develop high yielding okra varieties like in all other crop improvement. This is important for selecting parents in combination breeding and to obtain transgressive segregants[6]. The knowledge of pattern of inheritance of various characters are important consideration while, determining the most approximate breeding procedures applicable to any particular crop.

## **MATERIALS AND METHODS**

### **Experimental Site**

The experiment was conducted at the experimental field of Genetics and Plant Breeding Department of Sher-e-Bangla Agricultural University, Dhaka Bangladesh during March 2017 to July 2017.

### **Plant Materials**

Twenty eight genotypes of okra were used in this study which was collected from Bangladesh Agricultural Research Institute (BARI), Gazipur and local market (Table 1). G1-G17 were breeding line, the rest were commercial line.

## Experimental Design

The experiment was conducted in randomized complete block design with three replications. In each block, each genotype was planted in one row of 8.4 m length and 1 m width, maintaining a plant to plant spacing of 0.6 m and accommodated 14 plants per plot.

## Field Managements

The recommended dosage of Urea, Triple Super Phosphate (TSP), Muriate of Potash (MP) were applied in field at the rate of 150, 100, 150 Kg/ha respectively. Irrigation was applied once a week at emergence and every two weeks at flowering and pod production. Chemicals and cultural practices were applied to control insect pest.

## Observations recorded

Observations were recorded on five plants in each genotype in each replication for all the characters studied. The observations are given below-

Days to first flowering, Days to 50% flowering, Days to maturity, Plant height (cm), Number of primary branches per plant, Fruit character and yield, Fruit length (cm), Fruit diameter (mm), Average fruit weight (g), Number of tender fruits per plant, Number of seeds per pod, Hundred seed weight (g), Fruit yield per plant (g)

**Table 1. Details of Experimental Materials**

GENOTYPES	NAME OF GENOTYPES	SOURCE
G1	BARI Dheros1	Bangladesh Agricultural Research Institute
G2	BARI Dheros2	Bangladesh Agricultural Research Institute
G3	BD-1928	Bangladesh Agricultural Research Institute
G4	BD-1929	Bangladesh Agricultural Research Institute
G5	BD-1930	Bangladesh Agricultural Research Institute

G6	BD-1931	Bangladesh Institute	Agricultural	Research
G7	BD-1932	Bangladesh Institute	Agricultural	Research
G8	BD-1933	Bangladesh Institute	Agricultural	Research
G9	BD-1934	Bangladesh Institute	Agricultural	Research
G10	BD-1935	Bangladesh Institute	Agricultural	Research
G11	BD-1936	Bangladesh Institute	Agricultural	Research
G12	BD-1937	Bangladesh Institute	Agricultural	Research
G13	BD-1938	Bangladesh Institute	Agricultural	Research
G14	BD-1939	Bangladesh Institute	Agricultural	Research
G15	BD-1940	Bangladesh Institute	Agricultural	Research
G16	BD-1941	Bangladesh Institute	Agricultural	Research
G17	BD-1942	Bangladesh Institute	Agricultural	Research
G18	OrkaOnamika	Krishibid Seed Limited		
G19	Ladies Finger	Krishibid Seed Limited		
G20	Kohnur	Krishibid Seed Limited		
G21	Mukta	Krishibid Seed Limited		
G22	Soft Finger	Krishibid Seed Limited		
G23	KS-3	Krishibid Seed Limited		
G24	KS-1201	Krishibid Seed Limited		
G25	Shruti-16	Local Market		
G26	Preeti-72	Local Market		

G27	NF-1003	Local Market
G28	SONIYA-86	Local Market

### Statistical Analysis

Statistical Analysis was done by using GENSTAT 5.13 and Microsoft Excel 2007 software.

### Result and Discussions

#### Genetic distance

Genetic distance of 28 okra genotypes was measured using Euclidean distance based on 11 traits and the result is presented (Table 2). The genetic distances for all possible pairs of 28 okra genotypes ranged from 0.19 to 4.09 with mean and standard deviation of 1.47 and 0.66, respectively. The most distant genotypes were G1 and G28 (4.09) followed by G1 and G27 (3.32), G1 and G23 (3.60), G1 and G14 (3.37) and G1 and G17 (3.00). The lowest genetic distance was exhibited between G10 and G24 (0.19) followed by G10 and G22 (0.32), G10 and G20 (0.37), G6 and G20 (0.39) and G10 and G25 (0.39). This suggested that the higher chance of improving the crop production through collection, characterization, evaluation and selection or hybridization of okra genotypes from different regions even from other countries. The extent of diversity present between genotypes determines the extent of improvement gained through selection and hybridization. The more divergent the two genotypes are the more will be the probability of improving through selection and hybridization. This result is supported by Prakash et al, Kamalpreet et al.who reported that presence of genetic diversity for okra collection[6][7].

**Table 2. Genetic Euclidean distances and mean Euclidean distance of 28 genotypes based on 11 traits**

Genotypes	Squared Euclidean Distance														
	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15
G2	1.08														
G3	2.83	0.62													
G4	0.88	0.83	1.76												
G5	1.98	1.36	1.83	1.53											
G6	2.14	0.65	0.47	0.81	1.65										
G7	1.84	0.90	1.03	1.48	0.49	1.19									
G8	2.73	2.33	2.86	0.84	2.45	1.62	2.59								
G9	0.92	0.56	1.16	0.59	0.95	0.53	0.78	1.89							
G10	1.33	0.77	1.50	0.44	1.26	0.76	1.44	0.97	0.44						
G11	1.32	0.74	1.41	1.50	1.25	1.63	0.85	2.71	1.08	1.28					
G12	1.49	1.17	2.21	0.90	0.81	1.82	1.32	1.58	1.20	0.77	1.84				
G13	1.57	1.57	2.26	1.35	1.09	1.69	1.21	2.26	0.70	0.88	0.90	1.89			
G14	3.37	1.64	1.73	1.53	1.87	1.36	2.55	1.44	1.88	0.83	2.55	1.12	2.65		
G15	2.04	0.94	1.30	1.41	1.72	1.01	0.99	1.82	0.92	1.01	0.67	2.23	1.01	2.44	
G16	2.79	1.25	1.59	1.62	1.75	1.18	1.64	1.34	1.46	0.92	1.68	1.50	2.28	1.13	0.86
G17	3.00	1.09	0.76	2.09	0.88	0.99	0.55	2.44	1.16	1.39	1.19	1.74	1.70	1.73	0.79
G18	1.27	0.55	1.12	1.52	1.43	1.66	1.19	2.94	1.19	1.19	0.72	1.15	1.61	1.88	1.66
G19	3.09	1.83	1.99	2.56	0.55	2.04	0.78	2.74	1.53	1.69	1.67	1.44	1.64	2.17	1.42

G20	1.57	0.51	1.03	0.61	2.07	0.39	1.88	1.45	0.61	0.37	1.53	1.55	1.58	1.09	1.08
G21	1.51	0.58	1.24	1.40	0.52	1.10	0.52	2.89	0.44	0.93	0.93	1.13	1.02	2.03	1.04
G22	2.16	1.53	2.33	1.11	1.43	1.62	2.00	0.95	1.21	0.32	1.80	0.79	1.21	0.77	1.45
G23	3.60	1.44	0.98	2.06	1.37	0.66	1.62	2.56	1.27	1.43	2.20	2.30	2.15	1.25	1.66
G24	1.66	1.13	1.83	0.61	1.73	0.90	1.92	0.62	0.79	0.19	1.53	1.23	1.11	0.97	0.94
G25	1.59	1.46	2.22	0.68	1.25	1.40	1.45	0.46	0.98	0.39	1.38	0.82	1.00	1.27	1.03
G26	2.46	1.75	2.82	1.30	2.00	1.92	2.42	0.99	1.65	0.60	1.81	1.31	1.79	1.13	1.28
G27	3.32	2.14	2.00	2.02	2.65	1.64	2.90	1.53	1.94	0.97	2.17	2.24	2.09	0.89	1.86
G28	4.09	1.97	2.10	2.66	2.92	1.66	2.46	2.44	1.94	1.41	2.34	2.98	2.47	2.12	0.90

	G16	G17	G18	G19	G20	G21	G22	G23	G24	G25	G26	G27
G17	0.711											
G18	1.984	1.505										
G19	1.151	0.412	1.870									
G20	1.124	1.614	1.333	2.480								
G21	1.353	0.722	1.123	0.818	1.236							
G22	0.964	1.623	1.569	1.443	1.002	1.461						
G23	1.243	0.741	2.360	1.413	1.216	1.150	1.857					
G24	0.800	1.567	1.614	1.883	0.410	1.464	0.312	1.499				
G25	0.879	1.459	1.586	1.405	1.128	1.503	0.332	2.063	0.302			
G26	0.594	1.853	2.306	1.945	1.255	1.770	0.466	2.212	0.534	0.542		
G27	1.226	1.848	1.926	2.436	1.281	2.623	0.907	1.855	0.756	1.052	1.257	
G28	0.610	1.250	3.073	1.963	1.558	1.833	1.599	1.780	1.387	1.789	1.061	1.787

### **Contribution of different characters to total diversity**

The relative contribution of eleven different characters intakes in the evaluation of 28 genotypes towards the expression of genetic divergence is given in Table 3. The percent contribution of component characters ranged from 0.010 to 26.74 percent. The studies revealed that more or less contributions of similar characters towards total divergence was also been discussed by Dhaduk et al, Mamta and Choudhury, Patel et al, and Singh and Jain [8,9,10,11]

Principal components analysis (PCA) results of 11 quantitative traits are presented (Table 3). The PCA analysis results includes the factor scores of each character among the 28 okra accessions, Eigen values, percentage total variance accounted for by eight principal components (PCs). This principal component analysis resulted in eleven principal components (PC1 to PC11) with Eigen values ranged from 0.012 to 2.941. The eleven principal components accounted varied percentage of total variance ranged from 0.1 to 26.74%. Cumulative percent of total variation up to PCA five with eigen value more than unity accounted 80.67%. Ahiakpa, Nwangburuka et al and Mihretu et al who reported that principal component axes contributed 64.32%, 78.51% and 83% variation, respectively [12,13,14]. The first five components were retained in analysis because eigen values are >1. The others factors having eigen value < 1 were ignored. These were ignored due to Gutten's lower bound principle that eigen values <1 should be ignored [15].

The first three principal components PC1, PC2 and PC3 with values of 26.74%, 18.15% and 14.84%, respectively, contributed more to the total of 59.73% variation. Similar result was reported by Amoatey et al and Ahiakpa that the first principal component (PC1) recording the highest (32.44%) variance [12,16]. According to Chahal and Gosal, characters with largest absolute values closer to unity with in the first principal component influence the clustering more than those with lower absolute values closer to zero. [17]

**Table 3. Eigen values and yield percent contribution of 11 characters of 28 genotype**

Principal component axes	Eigen values	Percent variation	Cumulative % of percent variation
I	2.941	26.74	26.74
II	1.996	18.15	44.89
III	1.632	14.84	59.73
IV	1.292	11.75	71.48
V	1.011	9.19	80.67
VI	0.780	7.09	87.76
VII	0.690	6.28	94.04
VIII	0.297	2.70	96.74
IX	0.213	1.94	98.68
X	0.135	1.22	99.9
XI	0.012	0.10	100

### Conclusion

Results of the present studies indicated significant variation among the genotypes for all the characters studied. Plant height, fruits per plant and fruit weight contributed maximum towards fruit yield improvement. Twenty eight okra genotypes formed five different clusters. Considering genetic variability, diversity and other agronomic performance selection of genotypes G1 and G18 could be selected for earliness and high fruit yield and genotypes G6 and G20 selected for less seeds per fruit for future breeding program. High genotypic distance observed between G1 and G28, G27, G23, G14, G17, respectively.

### Disclaimer

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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